

SEQUENCE LISTING



<110> Guss, Bengt  
 Nilsson, Martin  
 Frykberg, Lars  
 Flock, Jan-Ingmar  
 Lindberg, Martin

<120> Fibrinogen Binding Protein Originating from  
 Coagulase-Negative Staphylococcus

<130> guss 09/147405

<140> 09/147405

<141> 1999-04-01

<150> PCT/SE97/10191

<151> 1997-06-18

<150> SE 9602496-3

<151> 1996-06-20

<160> 15

<170> PatentIn Ver. 2.0

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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22

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Sub  
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32

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<220>  
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gtg atc aat aat aat cag tca ata aac acc gac gat aat aac caa ata 95  
Val Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile  
20 25 30

att aaa aaa gaa gaa acg aat aac tac gat ggc ata gaa aaa cgc tca 143  
Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser  
35 40 45

gaa gat aga aca gag tca aca aca aat gta gat gaa aac gaa gca aca 191  
Glu Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr  
50 55 60

ttt tta caa aag acc cct caa gat aat act cat ctt aca gaa gaa gag 239  
Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu  
65 70 75

gta aaa gaa tcc tca tca gtc gaa tcc tca aat tca tca att gat act 287

Val	Lys	Glu	Ser	Ser	Ser	Val	Glu	Ser	Ser	Asn	Ser	Ser	Ile	Asp	Thr	
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gcc	caa	caa	cca	tct	cac	aca	aca	ata	aat	aga	gaa	gaa	tct	gtt	caa	335
Ala	Gln	Gln	Pro	Ser	His	Thr	Thr	Ile	Asn	Arg	Glu	Glu	Ser	Val	Gln	
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aca	agt	gat	aat	gta	gaa	gat	tca	cac	gta	tca	gat	ttt	gct	aac	tct	383
Thr	Ser	Asp	Asn	Val	Glu	Asp	Ser	His	Val	Ser	Asp	Phe	Ala	Asn	Ser	
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aaa	ata	aaa	gag	agt	aac	act	gaa	tct	ggg	aaa	gaa	gag	aat	act	ata	431
Lys	Ile	Lys	Glu	Ser	Asn	Thr	Glu	Ser	Gly	Lys	Glu	Glu	Asn	Thr	Ile	
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gag	caa	cct	aat	aaa	gta	aaa	gaa	gat	tca	aca	aca	agt	cag	ccg	tct	479
Glu	Gln	Pro	Asn	Lys	Val	Lys	Glu	Asp	Ser	Thr	Thr	Ser	Gln	Pro	Ser	
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ggc	tat	aca	aat	ata	gat	gaa	aaa	att	tca	aat	caa	gat	gag	tta	tta	527
Gly	Tyr	Thr	Asn	Ile	Asp	Glu	Lys	Ile	Ser	Asn	Gln	Asp	Glu	Leu	Leu	
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aat	tta	cca	ata	aat	gaa	tat	gaa	aat	aag	gct	aga	cca	tta	tct	aca	575
Asn	Leu	Pro	Ile	Asn	Glu	Tyr	Glu	Asn	Lys	Ala	Arg	Pro	Leu	Ser	Thr	
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Thr	Ser	Ala	Gln	Pro	Ser	Ile	Lys	Arg	Val	Thr	Val	Asn	Gln	Leu	Ala	
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gcg	gaa	caa	ggg	tcg	aat	gtt	aac	cat	tta	att	aaa	gtt	act	gat	caa	671
Ala	Glu	Gln	Gly	Ser	Asn	Val	Asn	His	Leu	Ile	Lys	Val	Thr	Asp	Gln	
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agt	att	act	gaa	gga	tat	gat	gat	agt	gaa	ggg	gtt	att	aaa	gca	cat	719
Ser	Ile	Thr	Glu	Gly	Tyr	Asp	Asp	Ser	Glu	Gly	Val	Ile	Lys	Ala	His	
		225				230					235					
gat	gct	gaa	aac	tta	atc	tat	gat	gta	act	ttt	gaa	gta	gat	gat	aag	767
Asp	Ala	Glu	Asn	Leu	Ile	Tyr	Asp	Val	Thr	Phe	Glu	Val	Asp	Asp	Lys	
240					245					250				255		
gtg	aaa	tct	ggg	gat	acg	atg	aca	gtg	gat	ata	gat	aag	aat	aca	gtt	815
Val	Lys	Ser	Gly	Asp	Thr	Met	Thr	Val	Asp	Ile	Asp	Lys	Asn	Thr	Val	
			260						265					270		
cca	tca	gat	tta	acc	gat	agc	ttt	aca	ata	cca	aaa	ata	aaa	gat	aat	863

Sub  
II

Pro Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn  
 275 280 285

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 Ser Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln  
 290 295 300

atc acc tat act ttt aca gat tat gta gat aag tat gaa aat att aaa 959  
 Ile Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn Ile Lys  
 305 310 315

gca cac ctt aaa tta acg tca tac att gat aaa tca aag gtt cca aat 1007  
 Ala His Leu Lys Leu Thr Ser Tyr Ile Asp Lys Ser Lys Val Pro Asn  
 320 325 330 335

aat aat acc aag tta gat gta gaa tat aaa acg gcc ctt tca tca gta 1055  
 Asn Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser Ser Val  
 340 345 350

aat aaa aca att acg gtt gaa tat caa aga cct aac gaa aat cgg act 1103  
 Asn Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn Arg Thr  
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gct aac ctt caa agt atg ttt aca aat ata gat acg aaa aat cat aca 1151  
 Ala Asn Leu Gln Ser Met Phe Thr Asn Ile Asp Thr Lys Asn His Thr  
 370 375 380

gtt gag caa acg att tat att aac cct ctt cgt tat tca gcc aag gaa 1199  
 Val Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu  
 385 390 395

aca aat gta aat att tca ggg aat ggt gat gaa ggt tca aca att ata 1247  
 Thr Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile  
 400 405 410 415

gac gat agc aca ata att aaa gtt tat aag gtt gga gat aat caa aat 1295  
 Asp Asp Ser Thr Ile Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn  
 420 425 430

tta cca gat agt aac aga att tat gat tac agt gaa tat gaa gat gtc 1343  
 Leu Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu Asp Val  
 435 440 445

aca aat gat gat tat gcc caa tta gga aat aat aat gat gtg aat att 1391  
 Thr Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val Asn Ile  
 450 455 460

aat ttt ggt aat ata gat tca cca tat att att aaa gtt att agt aaa 1439

Sub  
 I

Asn Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys  
 465 470 475

tat gac cct aat aag gat gat tac acg act ata cag caa act gtg aca 1487  
 Tyr Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr  
 480 485 490 495

atg cag acg act ata aat gag tat act ggt gag ttt aga aca gca tcc 1535  
 Met Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser  
 500 505 510

tat gat aat aca att gct ttc tct aca agt tca ggt caa gga caa ggt 1583  
 Tyr Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly  
 515 520 525

gac ttg cct cct gaa aaa act tat aaa atc gga gat tac gta tgg gaa 1631  
 Asp Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu  
 530 535 540

gat gtagat aaa gat ggt att caa aat aca aat gat aat gaa aaa ccg 1679  
 Asp Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro  
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ctt agt aat gta ttg gta act ttg acg tat cct gat gga act tca aaa 1727  
 Leu Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys  
 560 565 570 575

tca gtc aga aca gat gaa gat ggg aaa tat caa ttt gat ggg gtg cag 1775  
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<211> 593

<212> PRT

<213> Staphylococcus epidermidis

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Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu

35

40

45

Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe  
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 Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala  
 85 90 95  
 Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln Thr  
 100 105 110  
 Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser Lys  
 115 120 125  
 Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile Glu  
 130 135 140  
 Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly  
 145 150 155 160  
 Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn  
 165 170 175  
 Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr Thr  
 180 185 190  
 Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala Ala  
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 Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr Asp Gln Ser  
 210 215 220  
 Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp  
 225 230 235 240  
 Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys Val  
 245 250 255  
 Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val Pro  
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 Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn Ser  
 275 280 285  
 Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln Ile



290

295

300

Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn Ile Lys Ala  
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325 330 335

Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser Ser Val Asn  
340 345 350

Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn Arg Thr Ala  
355 360 365

Asn Leu Gln Ser Met Phe Thr Asn Ile Asp Thr Lys Asn His Thr Val  
370 375 380

Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr  
385 390 395 400

Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp  
405 410 415

Asp Ser Thr Ile Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn Leu  
420 425 430

Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu Asp Val Thr  
435 440 445

Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val Asn Ile Asn  
450 455 460

Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys Tyr  
465 470 475 480

Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr Met  
485 490 495

Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr  
500 505 510

Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly Asp  
515 520 525

Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp  
530 535 540

Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu

545                      550                      555                      560

Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser  
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accctcaag ataatactca tcttacagaa gaagaggtaa aagaatcctc atcagtcgaa 240
tcctcaaatt catcaattga tactgcccaa caaccatctc acacaacaat aaatagagaa 300
gaatctgttc aaacaagtga taatgtagaa gattcacacg tatcagattt tgctaactct 360
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aaagtaaaaag aagattcaac aacaagtcag ccgtctggct atacaaatat agatgaaaaa 480
atttcaaatac aagatgagtt attaaattta ccaataaatg aatatgaaaa taaggctaga 540
ccattatcta caacatctgc ccaaccatcg attaaacgtg taaccgtaaa tcaattagcg 600
gcggaacaag gttcgaatgt taaccattta attaaagtta ctgatcaaag tattactgaa 660
ggatatgatg atagtgaagg tggtattaaa gcacatgatg ctgaaaactt aatctatgat 720
gtaacttttg aagtagatga taaggtgaaa tctggtgata cgatgacagt ggatatagat 780
aagaatacag ttccatcaga tttaaccgat agctttacaa taccaaaaaat aaaagataat 840
tctggagaaa tcatcgctac aggtacttat gataacaaaa ataaacaaat cacctatact 900

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 ggtgatgaag gttcaacaat tatagacgat agcacaataa ttaaagttta taagggttga 1260  
 gataatcaaa atttaccaga tagtaacaga atttatgatt acagtgaata tgaagatgtc 1320  
 acaaatgatg attatgcca attaggaat aataatgatg tgaatattaa ttttggtaat 1380  
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 gacttgctc ctgaaaaaac ttataaaaac ggagattacg tatgggaaga tgtagataaa 1620  
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 Tyr Asp Gly Ile Glu Lys Arg Ser Glu Asp Arg Thr Glu Ser Thr Thr  
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 Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr Pro Gln Asp  
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Asn Thr His Leu Thr Glu Glu Glu Val Lys Glu Ser Ser Ser Val Glu  
 65 70 75 80  
 Ser Ser Asn Ser Ser Ile Asp Thr Ala Gln Gln Pro Ser His Thr Thr  
 85 90 95  
 Ile Asn Arg Glu Glu Ser Val Gln Thr Ser Asp Asn Val Glu Asp Ser  
 100 105 110  
 His Val Ser Asp Phe Ala Asn Ser Lys Ile Lys Glu Ser Asn Thr Glu  
 115 120 125  
 Ser Gly Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys Val Lys Glu  
 130 135 140  
 Asp Ser Thr Thr Ser Gln Pro Ser Gly Tyr Thr Asn Ile Asp Glu Lys  
 145 150 155 160  
 Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn Glu Tyr Glu  
 165 170 175  
 Asn Lys Ala Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro Ser Ile Lys  
 180 185 190  
 Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser Asn Val Asn  
 195 200 205  
 His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly Tyr Asp Asp  
 210 215 220  
 Ser Glu Gly Val Ile Lys Ala His Asp Ala Glu Asn Leu Ile Tyr Asp  
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 Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp Thr Met Thr  
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 Thr Ile Pro Lys Ile Lys Asp Asn Ser Gly Glu Ile Ile Ala Thr Gly  
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 Thr Tyr Asp Asn Lys Asn Lys Gln Ile Thr Tyr Thr Phe Thr Asp Tyr  
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 305 310 315 320

Sub  
Ty

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325 330 335

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Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile Tyr Ile Asn  
370 375 380

Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile Ser Gly Asn  
385 390 395 400

Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile Ile Lys Val  
405 410 415

Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn Arg Ile Tyr  
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Asp Tyr Ser Glu Tyr Glu Asp Val Thr Asn Asp Asp Tyr Ala Gln Leu  
435 440 445

Gly Asn Asn Asn Asp Val Asn Ile Asn Phe Gly Asn Ile Asp Ser Pro  
450 455 460

Tyr Ile Ile Lys Val Ile Ser Lys Tyr Asp Pro Asn Lys Asp Asp Tyr  
465 470 475 480

Thr Thr Ile Gln Gln Thr Val Thr Met Gln Thr Thr Ile Asn Glu Tyr  
485 490 495

Thr Gly Glu Phe Arg Thr Ala Ser Tyr Asp Asn Thr Ile Ala Phe Ser  
500 505 510

Thr Ser Ser Gly Gln Gly Gln Gly Asp Leu Pro Pro Glu Lys Thr Tyr  
515 520 525

Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Ile Gln  
530 535 540

Asn Thr Asn Asp Asn Glu Lys Pro Leu Ser Asn Val Leu Val Thr Leu  
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Lys Tyr Gln Phe Asp  
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<210> 14

<211> 3600

<212> DNA

<213> Staphylococcus epidermidis

<220>

<221> CDS

<222> (33)..(3308)

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Leu Leu Thr Lys Lys Lys Pro Ile Ala Asn Lys Ser Asn Lys Tyr Ala  
10 15 20

att aga aaa ttc aca gta ggt aca gcg tct att gta ata ggt gca aca 149  
Ile Arg Lys Phe Thr Val Gly Thr Ala Ser Ile Val Ile Gly Ala Thr  
25 30 35

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Leu Leu Phe Gly Leu Gly His Asn Glu Ala Lys Ala Glu Glu Asn Ser  
40 45 50 55

gta caa gac gtt aaa gat tcg aat acg gat gat gaa tta tca gac agc 245  
Val Gln Asp Val Lys Asp Ser Asn Thr Asp Asp Glu Leu Ser Asp Ser  
60 65 70

aat gat cag tct agt gat gaa gaa aag aat gat gtg atc aat aat aat 293  
Asn Asp Gln Ser Ser Asp Glu Glu Lys Asn Asp Val Ile Asn Asn Asn  
75 80 85

cag tca ata aac acc gac gat aat aac caa ata att aaa aaa gaa gaa 341  
Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile Ile Lys Lys Glu Glu  
90 95 100

acg aat aac tac gat ggc ata gaa aaa cgc tca gaa gat aga aca gag 389  
Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu Asp Arg Thr Glu  
105 110 115

tca aca aca aat gta gat gaa aac gaa gca aca ttt tta caa aag acc 437

Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr  
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 Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val Lys Glu Ser Ser  
 140 145 150  
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 Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala Gln Gln Pro Ser  
 155 160 165  
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 His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln Thr Ser Asp Asn Val  
 170 175 180  
 gaa gat tca cac gta tca gat ttt gct aac tct aaa ata aaa gag agt 629  
 Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser Lys Ile Lys Glu Ser  
 185 190 195  
 aac act gaa tct ggt aaa gaa gag aat act ata gag caa cct aat aaa 677  
 Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys  
 200 205 210 215  
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 Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly Tyr Thr Asn Ile  
 220 225 230  
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 Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro  
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 Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser  
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 Asn Val Asn His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly  
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 Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp Ala Glu Asn Leu  
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Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp  
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 Asp Val Glu Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr  
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 Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile  
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 Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile  
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 Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn  
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Sub  
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gat tcc gat agt gat tca gac tca ggc agt gat tcg gat tcc gat agt 3125  
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 Ser Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp Tyr Gly  
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Leu Leu Gly Lys Arg Arg Lys Asn Arg Lys Asn Lys Asn  
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Ser Ile Val Ile Gly Ala Thr Leu Leu Phe Gly Leu Gly His Asn Glu  
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Ala Lys Ala Glu Glu Asn Ser Val Gln Asp Val Lys Asp Ser Asn Thr  
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Asp Asp Glu Leu Ser Asp Ser Asn Asp Gln Ser Ser Asp Glu Glu Lys  
65 70 75 80

Asn Asp Val Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn  
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Gln Ile Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys  
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Arg Ser Glu Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu  
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Ala Thr Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu  
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Glu Glu Val Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile

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 Asp Thr Ala Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser  
                                  165                                   170                                   175  
 Val Gln Thr Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala  
                                  180                                   185                                   190  
 Asn Ser Lys Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn  
                                  195                                   200                                   205  
 Thr Ile Glu Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln  
                                  210                                   215                                   220  
 Pro Ser Gly Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu  
 225                                   230                                   235                                   240  
 Leu Leu Asn Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu  
                                  245                                   250                                   255  
 Ser Thr Thr Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln  
                                  260                                   265                                   270  
 Leu Ala Ala Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr  
                                  275                                   280                                   285  
 Asp Gln Ser Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys  
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 Ala His Asp Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp  
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 Asp Lys Val Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn  
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 Asp Asn Ser Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn  
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 Lys Gln Ile Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn  
                                  370                                   375                                   380  
 Ile Lys Ala His Leu Lys Leu Thr Ser Tyr Ile Asp Lys Ser Lys Val  
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 Pro Asn Asn Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser

405 410 415  
 Ser Val Asn Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn  
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 His Thr Val Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala  
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 Lys Glu Thr Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr  
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 Gln Asn Leu Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu  
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 Asp Val Thr Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val  
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 Asn Ile Asn Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile  
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 Ser Lys Tyr Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr  
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 Val Thr Met Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr  
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 Ala Ser Tyr Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly  
 580 585 590  
 Gln Gly Asp Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val  
 595 600 605  
 Trp Glu Asp Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu  
 610 615 620  
 Lys Pro Leu Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr  
 625 630 635 640  
 Ser Lys Ser Val Arg Thr Asp Glu Asp Gly Lys Tyr Gln Phe Asp Gly  
 645 650 655  
 Leu Lys Asn Gly Leu Thr Tyr Lys Ile Thr Phe Glu Thr Pro Glu Gly

Sub  
T

660

665

670

Tyr Thr Pro Thr Leu Lys His Ser Gly Thr Asn Pro Ala Leu Asp Ser  
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Glu Gly Asn Ser Val Trp Val Thr Ile Asn Gly Gln Asp Asp Met Thr  
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Ile Asp Ser Gly Phe Tyr Gln Thr Pro Lys Tyr Ser Leu Gly Asn Tyr  
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Val Trp Tyr Asp Thr Asn Lys Asp Gly Ile Gln Gly Asp Asp Glu Lys  
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Gly Ile Ser Gly Val Lys Val Thr Leu Lys Asp Glu Asn Gly Asn Ile  
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Leu Asn Ser Gly Asn Tyr Ile Val His Phe Asp Lys Pro Ser Gly Met  
770 775 780

Thr Gln Thr Thr Thr Asp Ser Gly Asp Asp Asp Glu Gln Asp Ala Asp  
785 790 795 800

Gly Glu Glu Val His Val Thr Ile Thr Asp His Asp Asp Phe Ser Ile  
805 810 815

Asp Asn Gly Tyr Tyr Asp Asp Glu Ser Asp Ser Asp Ser Asp Ser Asp  
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Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp  
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Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp

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 Leu Gly Asn Ser Ser Asp Lys Ser Thr Lys Asp Lys Leu Pro Asp Thr  
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 Lys Asn Lys Asn  
 1090

Sub  
 I-1  
 C1  
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